

Figure 1

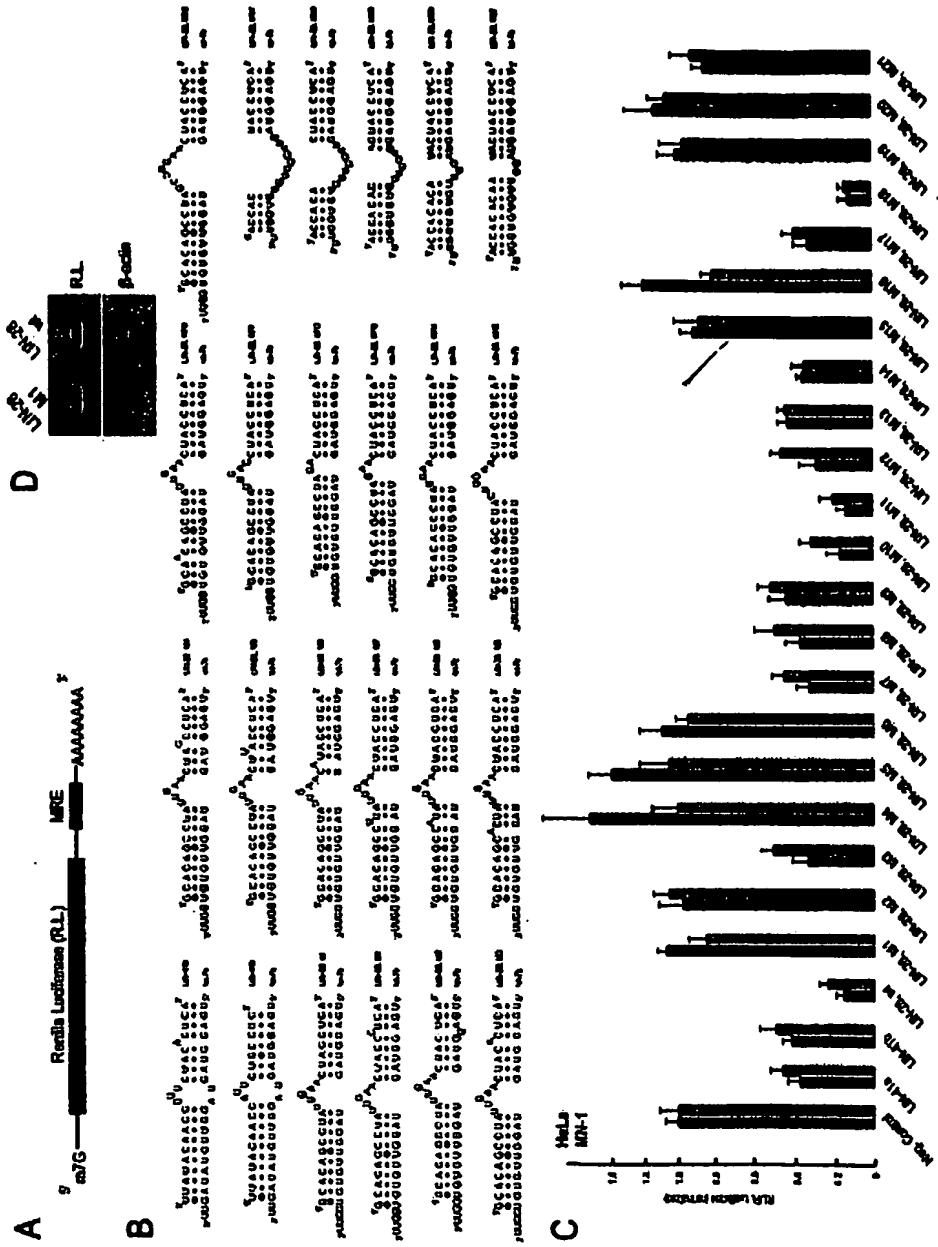
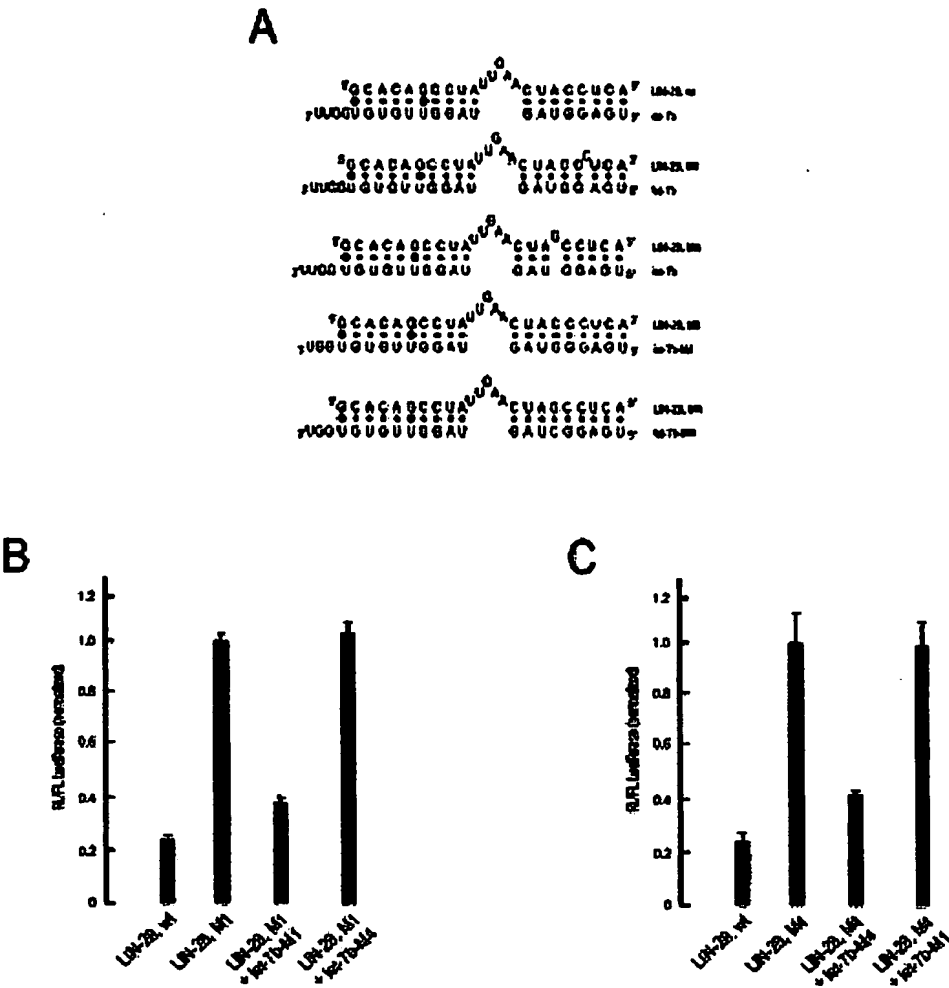


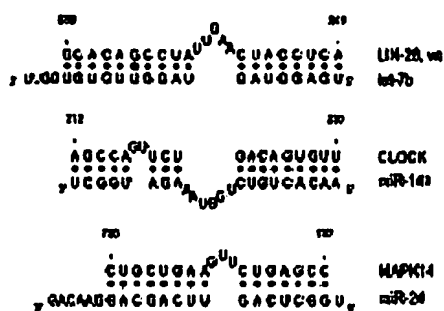
Figure 2



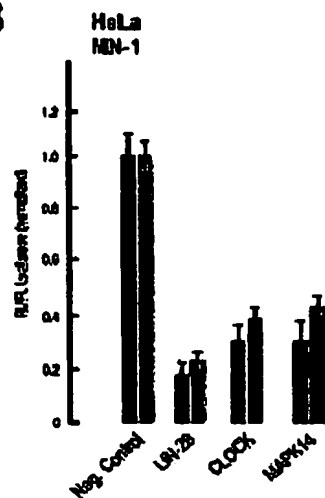
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Figure 3

A



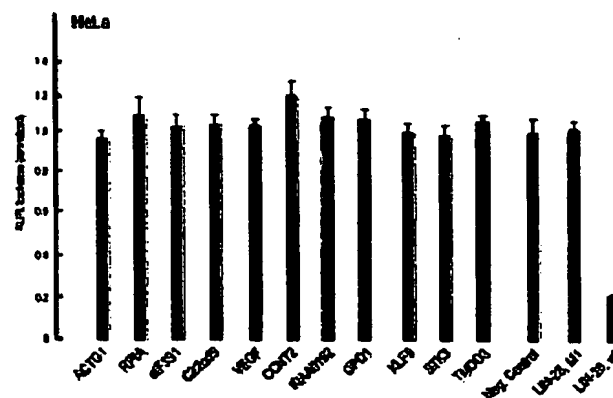
B



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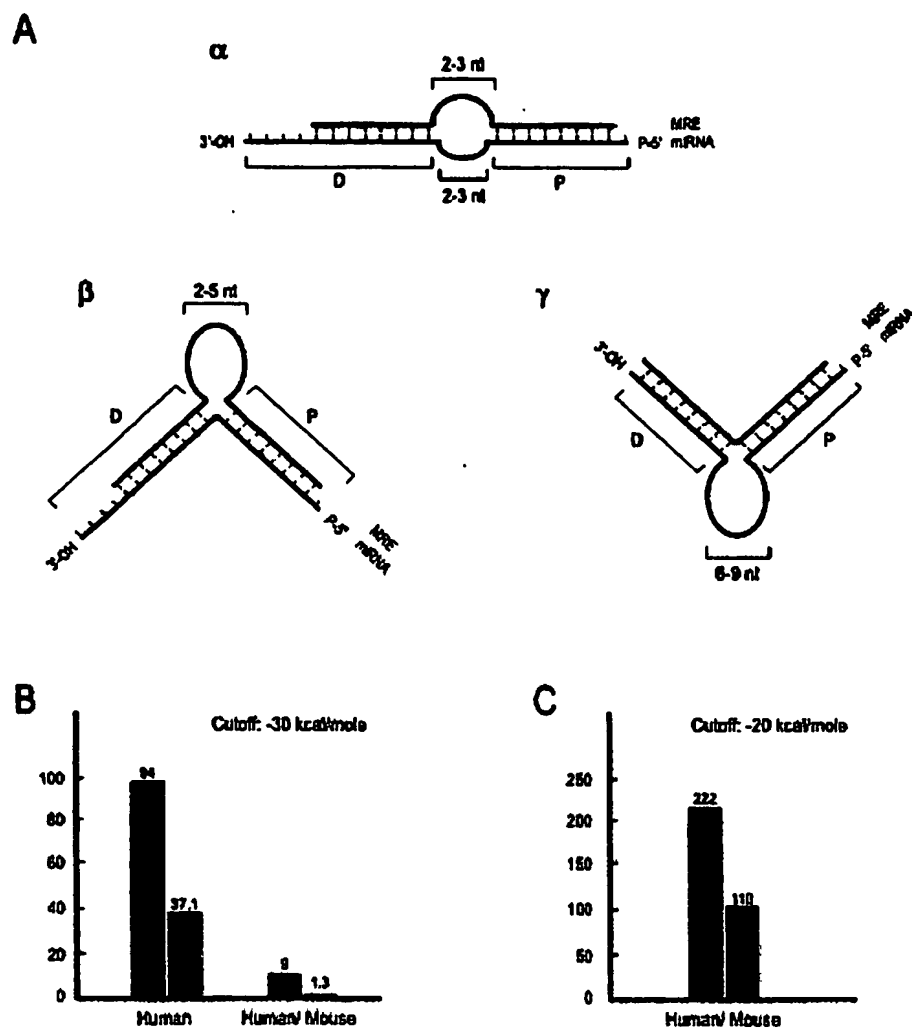
Figure 4

miRNA	Target Annotation	Site location miRNA 3' end	miRNA Binding Site (Top String: Target; Bottom String: miRNA)
let-7b	Actin gamma 1 (ACTG1; NM_001614)	1294	5' ---cagaca-cctcctcctagccca--- 3' 3' ---gtgtctctgga---cagc-ggagga--- 5'
let-7b	Ribose 5-phosphate isomerase A (RPIA; NM_144563)	1013	5' -----cacagccaggtctgacgtaccc--- 3' 3' ---ggtgtgtgga-----atg-atggag--- 5'
let-7c	Eucaryotic translation initiation factor 3, subunit 1 alpha (eIF3S1; NM_003758)	1140	5' ---atcagccttcaaccataccc--- 3' 3' ---tatgttggg---gg-atggag--- 5'
miR-15	Chromosome 22 open reading frame 5 (C22orf5; NM_012264)	3152	5' -----caggtca---aagtcctgct--- 3' 3' ---gtgttctgttaatacagagca--- 5'
miR-16	Vascular endothelial growth factor (VEGF; NM_003376)	1560	5' ---cgcacccctcattctctctgctgcca--- 3' 3' ---gcggt---tatataa---tgacagagagct--- 5'
miR-16	Cyclin T2 (CCNT2), transcript variant 2 (NM_001241)	2254	5' -----cactaccctctgctgctgctgct--- 3' 3' -----gggttatataa---tgacagagagca--- 5'
miR-24	KIAA0152 gene product (NM_014730)	4671	5' -----cactgct---cctgagcca--- 3' 3' ---gacagggagcgtcttgctcctggt--- 5'
miR-103	Glycerol-3-phosphate dehydrogenase 1 (soluble) (GPD1; NM_005276)	1368	5' ---cca-agccc---cagtcctgc--- 3' 3' ---ggttcctggggagctgctgctgag--- 5'
miR-141 (miR-157)	Kruppel-like factor 5 (intestinal) (KLF5; NM_001730)	2033	5' -----cactcatttactctgacagctgtc--- 3' 3' -----cgggtag---aat-ggtctgtcaaa--- 5'
miR-141 (miR-157)	Serine/threonine kinase 3 (STE20 homolog, yeast; STK3; NM_006281)	2756	5' ---gcaatctt---gacagctgc--- 3' 3' ---cgttagaagacggctcgtctacaa--- 5'
miR-145	Tropomodulin 3 (ubiquitous) (TMOD3; NM_014547)	1225	5' ---tctcctgggtgagagggagagagccgga--- 3' 3' ---aaggaacc---cttcgaccc--- 5'



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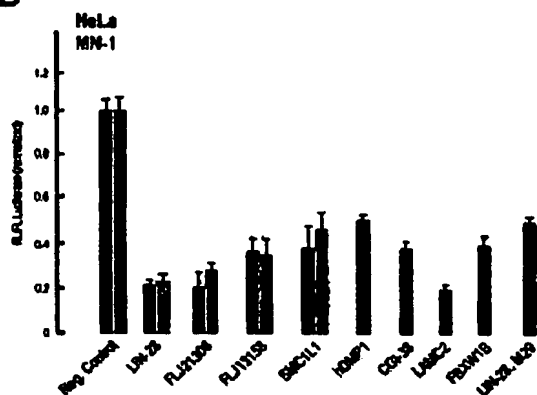
Figure 5.



[illegible]

2291 2373  
 A G C U U U U U U C A A U U U U C U 5'X7418  
 , A G U A U C G G A C A C U U U A C G A , 5'X7419  
 C A C A G A A C C U A U A C U A C U C A ' 5'X7420  
 , U U G U G U U G U U G U A U G A U G A G U , 5'X7421

**B**



C

$$\begin{array}{ccccccc}
 \text{UUUA}^{\text{U}}\text{CAAC}^{\text{U}} & & \text{CUAC}^{\text{U}}\text{UCA} & \text{---} & \text{UUUA}^{\text{U}}\text{CAAC}^{\text{U}} & \text{CUUC}^{\text{U}}\text{CUC} & \text{SMI(Ea)} \\
 \cdot \cdot \cdot & & \cdot \cdot \cdot \cdot \cdot & & \cdot \cdot \cdot \cdot \cdot & & \\
 \text{UUGAU}^{\text{U}}\text{AUGUUG}^{\text{U}} & & \text{CAUG}^{\text{U}}\text{CAU}^{\text{U}} & & \text{UUGAU}^{\text{U}}\text{AUGUUG}^{\text{U}} & & \text{CAUG}^{\text{U}}\text{CAU}^{\text{U}} \text{ MJE(Ea)}
 \end{array}$$

UUCAC UCUAGGGA G-28 (C4)  
 :GGG: :GGG: G-4 (C4)  
 ,AGUGU,AGAGUCCU,

CUCAUCAAAGC<sup>GA</sup> UUUUUAUA      229-23 (D.V.)  
 \*\*\*\*\*      \*\*\*\*\*  
 CGAGUAQUUUCG<sup>CG</sup> GACACUAA<sup>CG</sup>      231-22 (D.V.)

UC UAC CUCAGGUA 6-14 (C<sub>2</sub>)  
 , AGUGUG , GAGUCCU , 6-4 (C<sub>2</sub>)

GCUCA<sup>1</sup>UCAAAGC<sup>2</sup> A<sup>3</sup>UUUU<sup>4</sup>GAU      5' → 3'      3' → 5'  
 .....      .....  
 U<sup>5</sup>GAUU<sup>6</sup>AGUUU<sup>7</sup>U<sup>8</sup>C<sup>9</sup>A<sup>10</sup>GC<sup>11</sup>AG<sup>12</sup>AG<sup>13</sup>UAU<sup>14</sup>      3' → 5'      5' → 3'

UC CCG ACC UAC CUC A      RM-1 (2-37) (C.S.)  
 AGUAAAG CCG UCG AUGAGU      RM-241 (C.S.)

CAGC<sup>UUU</sup> AAUCA<sup>AC</sup> GUCUUCG<sup>G</sup>      orig  
GGG            CCGCC            GCGGC      10-17-68  
UGGUG... UGABU... CAGAAGCU      10-17-68

**Analysing 7 interaction predicted in Stark et al (2003)**

### hcyg-miR-7 interaction that abides by the miRNA Binding Rules

UCAB AA  
ACACGAAA CA AGUCUCCA Mary (Jury)  
..... ..  
170UUGUWU UA GU GACUADAAGGU, Mary? (Dun)



ACAGCAAAUACGCAAA      AGUGUUECA      157 (D.V.)  
     •••••      •••••  
     , UGUUGUUU      UCAGAAAGUU,      158 (D.V.)